SEQUENCE LISTING

<110> ST GEORGE'S HOSPITAL MEDICAL SCHOOL

<120> DIAGNOSTICS AND VACCINES FOR MYCOBACTERIAL INFECTIONS
      OF ANIMALS AND HUMANS

<130> N74368A DMG IJB DP

<140> PCT/ GB 99/ 00849
<141> 1999-03-18

<150> UK 9806093.2
<151> 1998-03-20

<160> 5

<170> PatentIn Ver. 2.1

<210> 1
<211> 1335
<212> DNA
<213> Mycobacterium avium

<400> 1
gtgactgaag ccaatgagtg caactcggcg tcgcgaaagg tttcagtcgc ggttgagcaa 60
gacaccgcaa gactactgga gtgcgtgcac aagcgccccc agctcgcggc tgaaagcgga 120
tgcaaagggg ttcgaagctt gagcaacatg cgaaggggag aacggcctat gagcctggga 180
caggttttcg acccgcgcgc gaatgcactt aatgcgtggc gcttggtgtt ggcgagcggg 240
gtgatcctat ggcattcgtt tccgctcact ggacgtatgc cgtgggcgcc gttcgtccag 300
ttgcttggcc ttggatgcgt tgatggtttc tttgcggtct ccggctatct catcgtctcg 360
agctggcttc gcaacccgca tcccgcccaa tacttcaccg ctcgatgtct tcgtattctc 420
ccgggtctgt ggatctgtct catcttgacg gcgtttgtca tcgctccgat aggtgtgggc 480
gcccagggcg gttcggccgc gaaactactg atgtccggcg ctccgatcga gtatgtgcta 540
aaagacagtg cggtttggat ggttaagttc gatatcggtg gcacacctcg cgatattcca 600
gttgcgggta tttggaacgg ttctctgtgg acattgggtt gggaggtgct ttgctatatc 660
ggcgtagcag tatttggtat gctcggactt cttagtcgcc gttggttcgt tccagggata 720
ttgatcctgg cgctgtcgtg gtcggtgttc ttgccggcat ggggcggaat acacgcgatc 780
gcctccaatg ctgcgcgatt cgctgtgatg ttttcggccg gagcgttgct gtatcaattc 840
cgtaacgtga ttccggctcg gtggtccttc gttgccgtcg gcctcattat cgttgtggtt 900
tcctctgccg tgctgccgga ctaccggttg gtggcggccc ttccgatggc gtacctaatc 960
atcgcttcgg gttcgctcat ccacaatcaa aggatgaggt tccgcaccga tctatcctat 1020
ggagtatata tttatgcgtt tccaattcag caagtgctgg tcctgtgtgg attcgccgag 1080
ataaatccaa tcgctttctg cgcgatttct gtcgcagcta ttttgccgct cgccgcgctc 1140
agttggttct tggtcgagaa acctgcgttg tcctggaaga gtcgtctccg gcggaaaaac 1200
agttcaattg cgctagccaa tatggaagat ggtggatcag tcggccgctc aaatgacatt 1260
cccggaaggc gggcccgctt tattggcgag aaagccgaag atcctcccgc gccgagccca 1320
agaccggctt tgtaa   1335

<210> 2
<211> 444
<212> PRT
<213> Mycobacterium avium

<400> 2

```
Val Thr Glu Ala Asn Glu Cys Asn Ser Ala Ser Arg Lys Val Ser Val
 1               5                  10                  15

Ala Val Glu Gln Asp Thr Ala Arg Leu Leu Glu Cys Val His Lys Arg
                20                  25                  30

Pro Gln Leu Ala Ala Glu Ser Gly Cys Lys Gly Val Arg Ser Leu Ser
            35                  40                  45

Asn Met Arg Arg Gly Glu Arg Pro Met Ser Leu Gly Gln Val Phe Asp
        50                  55                  60

Pro Arg Ala Asn Ala Leu Asn Ala Trp Arg Leu Val Leu Ala Ser Gly
65                  70                  75                  80

Val Ile Leu Trp His Ser Phe Pro Leu Thr Gly Arg Met Pro Trp Ala
                85                  90                  95

Pro Phe Val Gln Leu Leu Gly Leu Gly Cys Val Asp Gly Phe Phe Ala
            100                 105                 110

Val Ser Gly Tyr Leu Ile Val Ser Ser Trp Leu Arg Asn Pro His Pro
            115                 120                 125

Ala Gln Tyr Phe Thr Ala Arg Cys Leu Arg Ile Leu Pro Gly Leu Trp
    130                 135                 140

Ile Cys Leu Ile Leu Thr Ala Phe Val Ile Ala Pro Ile Gly Val Gly
145                 150                 155                 160

Ala Gln Gly Gly Ser Ala Ala Lys Leu Leu Met Ser Gly Ala Pro Ile
                165                 170                 175

Glu Tyr Val Leu Lys Asp Ser Ala Val Trp Met Val Lys Phe Asp Ile
            180                 185                 190

Gly Gly Thr Pro Arg Asp Ile Pro Val Ala Gly Ile Trp Asn Gly Ser
            195                 200                 205

Leu Trp Thr Leu Gly Trp Glu Val Leu Cys Tyr Ile Gly Val Ala Val
    210                 215                 220

Phe Gly Met Leu Gly Leu Leu Ser Arg Arg Trp Phe Val Pro Gly Ile
225                 230                 235                 240

Leu Ile Leu Ala Leu Ser Trp Ser Val Phe Leu Pro Ala Trp Gly Gly
                245                 250                 255

Ile His Ala Ile Ala Ser Asn Ala Ala Arg Phe Ala Val Met Phe Ser
            260                 265                 270

Ala Gly Ala Leu Leu Tyr Gln Phe Arg Asn Val Ile Pro Ala Arg Trp
```

Ser Phe Val Ala Val Gly Leu Ile Ile Val Val Val Ser Ser Ala Val
   290   295   300

Leu Pro Asp Tyr Arg Leu Val Ala Ala Leu Pro Met Ala Tyr Leu Ile
305   310   315   320

Ile Ala Ser Gly Ser Leu Ile His Asn Gln Arg Met Arg Phe Arg Thr
                325   330   335

Asp Leu Ser Tyr Gly Val Tyr Ile Tyr Ala Phe Pro Ile Gln Gln Val
                340   345   350

Leu Val Leu Cys Gly Phe Ala Glu Ile Asn Pro Ile Ala Phe Cys Ala
                355   360   365

Ile Ser Val Ala Ala Ile Leu Pro Leu Ala Ala Leu Ser Trp Phe Leu
   370   375   380

Val Glu Lys Pro Ala Leu Ser Trp Lys Ser Arg Leu Arg Arg Lys Asn
385   390   395   400

Ser Ser Ile Ala Leu Ala Asn Met Glu Asp Gly Gly Ser Val Gly Arg
                405   410   415

Ser Asn Asp Ile Pro Gly Arg Arg Ala Arg Phe Ile Gly Glu Lys Ala
                420   425   430

Glu Asp Pro Pro Ala Pro Ser Pro Arg Pro Ala Leu
                435   440

<210> 3
<211> 2543
<212> DNA
<213> Mycobacterium avium

<400> 3
atgcactgtc aatggccaag tagaagtccc cgctggtggc cagcagaagt ccccactccg 60
ctgcgggtgg ttggctaatt cttggcggct cccttcttgt ggtcggcgtg gcgcatccgg 120
taggactcgc cggaggtgac gacgatgctg gcgtggtgca gcagccgatc gaggatgctg 180
gcggcggtgg tgtgctcggg caggaatcgc ccccattgtt cgaagggcca atgcgaggcg 240
atggccaggg agcggcgctc gtagccggca gccacgagcc ggaacaacag ttgagtcccg 300
gtgtcgtcga gcggggcgaa gccgatctcg tccaagatga ccagatccgc gcggagcagg 360
gtgtcgatga tcttgccgac ggtgttgtcg gccaggccgc ggtagaggac ctcgatcagg 420
tcggcggcgg tgaagtagcg gactttgaat ccggcgtgga cggcagcgtg cccgcagccg 480
atgagcaggt gactttttgcc cgtaccaggt gggccaatga ccgccaggtt ctgttgtgcc 540
cgaatccatt ccaggctcga caggtagtcg aacgtggctg cggtgatcga cgatccggtg 600
acgtcgaacc cgtcgagggt cttggtgacc gggaaggctg cggccttgag acggttggcg 660
gtgttggagg catcgcgggc agcgatctcg gcctcaacca acgtccgcag gatctcctcc 720
ggtgtccagc gttgcgtctt ggcgacttgc aacacctcgg cggcgttgcg gcgcaccgtg 780
gccagcttca accgccgcag cgccgcgtca aggtcagcag ccagcggtgc cgccgaggac 840

```
ggtgccaccg gcttggcagc ggtggtcatg aggccgtccc gtcggtggtg ttgatcttgt 900
aggcctccaa cgagcgggtc tcgacggtgg gcagatcgag cacgagtgcg tcgccggcgg 960
ggcgggggttg tggggtgccg gcgccggcgg ccaggatcga gcgcacgtcg gcagcgcgga 1020
accggcgaaa cgcaaccgcc cggcgcagcg cgtcaatcaa agcctgttcg ccgtgggcgg 1080
cgccaaggcc gagcagaatg tcgagttcgg atttcagtcg ggtgttgccg atcgcagcag 1140
caccgacgag gaactgctgc gcttcggttc ccaatgcgca gaatcgtttc tctgcttggg 1200
ttttcgggcg aggaccacgc gagggtgcgg gtctgggtcc gtcgtagtgt tcatcgagga 1260
tggacacctc acctgggctg acgagctcgt gctcggccac gatcacaccg gtcgcaggtt 1320
ccaacaggat cagggcgcca tgatcgacca ccaccgccac ggtggcaccg acgagccgct 1380
gaggcaccga gtaacgagct gagccgtaac ggatgcacga gaggccgtcg accttacggc 1440
gcaccgaccc cgagccgatc gtcggccgca gcgagggcag ctccctcaag acggtgcgct 1500
cgtcaaccaa gcgatcgttg ggcacggcgc agatctccga gtggaccgtg gcattgacct 1560
cggcgcacca tagttgcgcc tgggcgttga gggcacgtag gtcgacctgc tcaccggcta 1620
acgcagcttc ggtcagcagc ggcaccgcaa ggtcgtcctg agcgtagcca cagaggttct 1680
ccacgatgcc cttcgattgc ggatccgcac cgtggcagaa gtccggaacg aagccatagt 1740
gggacgcgaa tcgcacataa tccggtgttg gaacaacaac attggcgacg acaccacctt 1800
tgaggcagcc catccggtcg gccaggatct tggccggaac cccaccgatc gcctcgaggg 1860
cttcggctat catcgcctgc gtggtcgagg ctttctcgtc ggcggcgaac cgctcaaacc 1920
gccaccgcga ataggccagc tccgcgcata acaccatcag ccccggtgcc gcttcggccc 1980
aatccatcac cagatagtca ccgggtgacc agaccgccgg acggcgttga tgccggttag 2040
cgttgcgcca ccatacttcc tgctcggcta ccaggcggcg gaagttacgg gccgagccct 2100
gatacccggc agctcgggcg atcggcagca tccgcttcgc cgacatcttg ccgtgtgatt 2160
tctcgactcg ggtggcgact agatcggtga acgcgtcgag gttgcgtggc cgtggttccc 2220
gcgggggcgc gccaccggcc tcggcccgct cgatgacccg cttgaccgtc ttgtgcgtac 2280
taccgcacag ctcggccgcg ccgcgatacg acccgacctg gtgatacgcc gaaatgatgt 2340
tcatacgctc ccttgcagac ttcaatagag ctccctgggc ggtgatcaag tgacagttgg 2400
cgctatcacc gtcaccgccc aggccctcag ctcccggaaa agacacgacg agcccgctaa 2460
ggagtgggga cttctacctg gccaccagtg gggacttcct actggccaca gatggggact 2520
ttctcatggc catggacatg cac                                         2543

<210> 4
<211> 2543
<212> DNA
<213> Mycobacterium avium

<400> 4
gtgcatgtcc atggccatga gaaagtcccc atctgtggcc agtaggaagt ccccactggt 60
ggccaggtag aagtcccccac tccttagcgg gctcgtcgtg tcttttccgg gagctgaggg 120
cctgggcggt gacggtgata gcgccaactg tcacttgatc accgcccagg gagctctatt 180
gaagtctgca agggagcgta tgaacatcat ttcggcgtat caccaggtcg ggtcgtatcg 240
cggcgcggcc gagctgtgcg gtagtacgca caagacggtc aagcgggtca tcgagcgggc 300
cgaggccggt ggcgcgcccc cgcgggaacc acggccacgc aacctcgacg cgttcaccga 360
tctagtcgcc acccgagtcg agaaatcaca cggcaagatg tcggcgaagc ggatgctgcc 420
gatcgcccga gctgccgggt atcagggctc ggcccgtaac ttccgccgcc tggtagccga 480
gcaggaagta tggtggcgca acgctaaccg gcatcaacgc cgtccggcgg tctggtcacc 540
cggtgactat ctggtgatgg attgggccga agcggcaccg gggctgatgg tgttatgcgc 600
ggagctggcc tattcgcggt ggcggtttga gcggttcgcc gccgacgaga aagcctcgac 660
cacgcaggcg atgatagccg aagccctcga ggcgatcggt ggggttccgg ccaagatcct 720
ggccgaccgg atgggctgcc tcaaaggtgg tgtcgtcgcc aatgttgttg ttccaacacc 780
ggattatgtg cgattcgcgt cccactatgg cttcgttccg gacttctgcc acggtgcgga 840
tccgcaatcg aagggcatcg tggagaacct ctgtggctac gctcaggacg accttgcggt 900
gccgctgctg accgaagctg cgttagccgg tgagcaggtc gacctacgtg ccctcaacgc 960
ccaggcgcaa ctatggtgcg ccgaggtcaa tgccacggtc cactcggaga tctgcgccgt 1020
```

```
gcccaacgat cgcttggttg acgagcgcac cgtcttgagg gagctgccct cgctgcggcc 1080
gacgatcggc tcggggtcgg tgcgccgtaa ggtcgacggc ctctcgtgca tccgttacgg 1140
ctcagctcgt tactcggtgc ctcagcggct cgtcggtgcc accgtggcgg tggtggtcga 1200
tcatggcgcc ctgatcctgt tggaacctgc gaccggtgtg atcgtggccg agcacgagtc 1260
cgtcagccca ggtgaggtgt ccatcctcga tgaacactac gacggaccca gacccgcacc 1320
ctcgcgtggt cctcgcccga aaacccaagc agagaaacga ttctgcgcat tgggaaccga 1380
agcgcagcag ttcctcgtcg gtgctgctgc gatcggcaac acccgactga aatccgaact 1440
cgacattctg ctcggccttg cgccgcccca cggcgaacag gctttgattg acgcgctgcg 1500
ccgggcggtt gcgtttcgcc ggttccgcgc tgccgacgtg cgctcgatcc tggccgccgg 1560
cgccggcacc ccacaacccc gccccgccgg cgacgcactc gtgctcgatc tgcccaccgt 1620
cgagacccgc tcgttggagg cctacaagat caacaccacc gacgggacgg cctcatgacc 1680
accgctgcca agccggtggc accgtcctcg gcggcaccgc tggctgctga ccttgacgcg 1740
gcgctgcggc ggttgaagct ggccacggtg cgccgcaacg ccgccgaggt gttgcaagtc 1800
gccaagacgc aacgctggac accggaggag atcctgcgga cgttggttga ggccgagatc 1860
gctgcccgcg atgcctccaa caccgccaac cgtctcaagg ccgcagcctt cccggtcacc 1920
aagaccctcg acgggttcga cgtcaccgga tcgtcgatca ccgcagccac gttcgactac 1980
ctgtcgagcc tggaatggat tcgggcacaa cagaacctgg cggtcattgg cccacctggt 2040
acgggcaaaa gtcacctgct catcggctgc gggcacgctg ccgtccacgc cggattcaaa 2100
gtccgctact tcaccgccgc cgacctgatc gaggtcctct accgcggcct ggccgacaac 2160
accgtcggca agatcatcga caccctgctc cgcgcggatc tggtcatctt ggacgagatc 2220
ggcttcgccc cgctcgacga caccgggact caactgttgt tccggctcgt ggctgccggc 2280
tacgagcgcc gctccctggc catcgcctcg cattggccct tcgaacaatg ggggcgattc 2340
ctgcccgagc acaccaccgc cgccagcatc ctcgatcggc tgctgcacca cgccagcatc 2400
gtcgtcacct ccggcgagtc ctaccggatg cgccacgccg accacaagaa gggagccgcc 2460
aagaattagc caaccacccg cagcggagtg gggacttctg ctggccacca gcggggactt 2520
ctacttggcc attgacagtg cat                                         2543

<210> 5
<211> 526
<212> PRT
<213> Mycobacterium avium

<400> 5
Val Ser Phe Pro Gly Ala Glu Gly Leu Gly Gly Asp Gly Asp Ser Ala
1               5                   10                  15

Asn Cys His Leu Ile Thr Ala Gln Gly Ala Leu Leu Lys Ser Ala Arg
            20                  25                  30

Glu Arg Met Asn Ile Ile Ser Ala Tyr His Gln Val Gly Ser Tyr Arg
        35                  40                  45

Gly Ala Ala Glu Leu Cys Gly Ser Thr His Lys Thr Val Lys Arg Val
    50                  55                  60

Ile Glu Arg Ala Glu Ala Gly Gly Ala Pro Pro Arg Glu Pro Arg Pro
65                  70                  75                  80

Arg Asn Leu Asp Ala Phe Thr Asp Leu Val Ala Thr Arg Val Glu Lys
                85                  90                  95

Ser His Gly Lys Met Ser Ala Lys Arg Met Leu Pro Ile Ala Arg Ala
            100                 105                 110
                                                        ?
```

```
Ala Gly Tyr Gln Gly Ser Ala Arg Asn Phe Arg Arg Leu Val Ala Glu
        115             120             125

Gln Glu Val Trp Trp Arg Asn Ala Asn Arg His Gln Arg Arg Pro Ala
        130             135             140

Val Trp Ser Pro Gly Asp Tyr Leu Val Met Asp Trp Ala Glu Ala Ala
145             150             155             160

Pro Gly Leu Met Val Leu Cys Ala Glu Leu Ala Tyr Ser Arg Trp Arg
                165             170             175

Phe Glu Arg Phe Ala Ala Asp Glu Lys Ala Ser Thr Thr Gln Ala Met
                180             185             190

Ile Ala Glu Ala Leu Glu Ala Ile Gly Gly Val Pro Ala Lys Ile Leu
        195             200             205

Ala Asp Arg Met Gly Cys Leu Lys Gly Gly Val Val Ala Asn Val Val
        210             215             220

Val Pro Thr Pro Asp Tyr Val Arg Phe Ala Ser His Tyr Gly Phe Val
225             230             235             240

Pro Asp Phe Cys His Gly Ala Asp Pro Gln Ser Lys Gly Ile Val Glu
                245             250             255

Asn Leu Cys Gly Tyr Ala Gln Asp Asp Leu Ala Val Pro Leu Leu Thr
                260             265             270

Glu Ala Ala Leu Ala Gly Glu Gln Val Asp Leu Arg Ala Leu Asn Ala
        275             280             285

Gln Ala Gln Leu Trp Cys Ala Glu Val Asn Ala Thr Val His Ser Glu
        290             295             300

Ile Cys Ala Val Pro Asn Asp Arg Leu Val Asp Glu Arg Thr Val Leu
305             310             315             320

Arg Glu Leu Pro Ser Leu Arg Pro Thr Ile Gly Ser Gly Ser Val Arg
                325             330             335

Arg Lys Val Asp Gly Leu Ser Cys Ile Arg Tyr Gly Ser Ala Arg Tyr
                340             345             350

Ser Val Pro Gln Arg Leu Val Gly Ala Thr Val Ala Val Val Val Asp
        355             360             365

His Gly Ala Leu Ile Leu Leu Glu Pro Ala Thr Gly Val Ile Val Ala
        370             375             380

Glu His Glu Leu Val Ser Pro Gly Glu Val Ser Ile Leu Asp Glu His
385             390             395             400
```

```
Tyr Asp Gly Pro Arg Pro Ala Pro Ser Arg Gly Pro Arg Pro Lys Thr
            405             410             415

Gln Ala Glu Lys Arg Phe Cys Ala Leu Gly Thr Glu Ala Gln Gln Phe
            420             425             430

Leu Val Gly Ala Ala Ala Ile Gly Asn Thr Arg Leu Lys Ser Glu Leu
        435             440             445

Asp Ile Leu Leu Gly Leu Gly Ala Ala His Gly Glu Gln Ala Leu Ile
    450             455             460

Asp Ala Leu Arg Arg Ala Val Ala Phe Arg Arg Phe Arg Ala Ala Asp
465             470             475             480

Val Arg Ser Ile Leu Ala Ala Gly Ala Gly Thr Pro Gln Pro Arg Pro
            485             490             495

Ala Gly Asp Ala Leu Val Leu Asp Leu Pro Thr Val Glu Thr Arg Ser
            500             505             510

Leu Glu Ala Tyr Lys Ile Asn Thr Thr Asp Gly Thr Ala Ser
            515             520             525
```

SEQUENCE LISTINGS

Sequence ID No.1

Total bases = 1,335

1	GTGACTGAAGCCAATGAGTGCAACTCGGCGTCGCGAAAGGTTTCAGTCGC
51	GGTTGAGCAAGACACCGCAAGACTACTGGAGTGCGTGCACAAGCGCCCCC
101	AGCTCGCGGCTGAAAGCGGATGCAAAGGGGTTCGAAGCTTGAGCAACATG
151	CGAAGGGGAGAACGGCCTATGAGCCTGGGACAGGTTTTCGACCCGCGCGC
201	GAATGCACTTAATGCGTGGCGCTTGGTGTTGGCGAGCGGGGTGATCCTAT
251	GGCATTCGTTTCCGCTCACTGGACGTATGCCGTGGGCGCCGTTCGTCCAG
301	TTGCTTGGCCTTGGATGCGTTGATGGTTTCTTTGCGGTCTCCGGCTATCT
351	CATCGTCTCGAGCTGGCTTCGCAACCCGCATCCCGCCCAATACTTCACCG
401	CTCGATGTCTTCGTATTCTCCCGGGTCTGTGGATCTGTCTCATCTTGACG
451	GCGTTTGTCATCGCTCCGATAGGTGTGGGCGCCCAGGGCGGTTCGGCCGC
501	GAAACTACTGATGTCCGGCGCTCCGATCGAGTATGTGCTAAAAGACAGTG
551	CGGTTTGGATGGTTAAGTTCGATATCGGTGGCACACCTCGCGATATTCCA
601	GTTGCGGGTATTTGGAACGGTTCTCTGTGGACATTGGGTTGGGAGGTGCT
651	TTGCTATATCGGCGTAGCAGTATTTGGTATGCTCGGACTTCTTAGTCGCC
701	GTTGGTTCGTTCCAGGGATATTGATCCTGGCGCTGTCGTGGTCGGTGTTC
751	TTGCCGGCATGGGGCGGAATACACGCGATCGCCTCCAATGCTGCGCGATT
801	CGCTGTGATGTTTTCGGCCGGAGCGTTGCTGTATCAATTCCGTAACGTGA
851	TTCCGGCTCGGTGGTCCTTCGTTGCCGTCGGCCTCATTATCGTTGTGGTT
901	TCCTCTGCCGTGCTGCCGGACTACCGGTTGGTGGCGGCCCTTCCGATGGC
951	GTACCTAATCATCGCTTCGGGTTCGCTCATCCACAATCAAAGGATGAGGT
1001	TCCGCACCGATCTATCCTATGGAGTATATATTTATGCGTTTCCAATTCAG
1051	CAAGTGCTGGTCCTGTGTGGATTCGCCGAGATAAATCCAATCGCTTTCTG
1101	CGCGATTTCTGTCGCAGCTATTTTGCCGCTCGCCGCGCTCAGTTGGTTCT
1151	TGGTCGAGAAACCTGCGTTGTCCTGGAAGAGTCGTCTCCGGCGGAAAAAC

SUBSTITUTE SHEET (RULE 26)

```
1201    AGTTCAATTGCGCTAGCCAATATGGAAGATGGTGGATCAGTCGGCCGCTC

1251    AAATGACATTCCCGGAAGGCGGGCCCGCTTTATTGGCGAGAAAGCCGAAG

1301    ATCCTCCCGCGCCGAGCCCAAGACCGGCTTTGTAA
```

5

Sequence ID No.2

Total Residues = 444

10
```
  1     VTEANECNSASRKVSVAVEQDTARLLECVHKRPQLAAESGCKGVRSLSNM

 51     RRGERPMSLGQVFDPRANALNAWRLVLASGVILWHSFPLTGRMPWAPFVQ

101     LLGLGCVDGFFAVSGYLIVSSWLRNPHPAQYFTARCLRILPGLWICLILT

151     AFVIAPIGVGAQGGSAAKLLMSGAPIEYVLKDSAVWMVKFDIGGTPRDIP

201     VAGIWNGSLWTLGWEVLCYIGVAVFGMLGLLSRRWFVPGILILALSWSVF
```
15
```
251     LPAWGGIHAIASNAARFAVMFSAGALLYQFRNVIPARWSFVAVGLIIVVV

301     SSAVLPDYRLVAALPMAYLIIASGSLIHNQRMRFRTDLSYGVYIYAFPIQ

351     QVLVLCGFAEINPIAFCAISVAAILPLAALSWFLVEKPALSWKSRLRRKN

401     SSIALANMEDGGSVGRSNDIPGRRARFIGEKAEDPPAPSPRPAL
```

20

Sequence ID No. 3 = IS1612 positive strand.


```
  1     ATGCACTGTCAATGGCCAAGTAGAAGTCCCCGCTGGTGGCCAGCAGAAGT

 51     CCCCACTCCGCTGCGGGTGGTTGGCTAATTCTTGGCGGCTCCCTTCTTGT
```
25
```
101     GGTCGGCGTGGCGCATCCGGTAGGACTCGCCGGAGGTGACGACGATGCTG

151     GCGTGGTGCAGCAGCCGATCGAGGATGCTGGCGGCGGTGGTGTGCTCGGG

201     CAGGAATCGCCCCCATTGTTCGAAGGGCCAATGCGAGGCGATGGCCAGGG

251     AGCGGCGCTCGTAGCCGGCAGCCACGAGCCGGAACAACAGTTGAGTCCCG

301     GTGTCGTCGAGCGGGGCGAAGCCGATCTCGTCCAAGATGACCAGATCCGC
```
30
```
351     GCGGAGCAGGGTGTCGATGATCTTGCCGACGGTGTTGTCGGCCAGGCCGC
```

401 GGTAGAGGACCTCGATCAGGTCGGCGGCGGTGAAGTAGCGGACTTTGAAT

451 CCGGCGTGGACGGCAGCGTGCCCGCAGCCGATGAGCAGGTGACTTTTGCC

501 CGTACCAGGTGGGCCAATGACCGCCAGGTTCTGTTGTGCCCGAATCCATT

551 CCAGGCTCGACAGGTAGTCGAACGTGGCTGCGGTGATCGACGATCCGGTG

601 ACGTCGAACCCGTCGAGGGTCTTGGTGACCGGGAAGGCTGCGGCCTTGAG

651 ACGGTTGGCGGTGTTGGAGGCATCGCGGGCAGCGATCTCGGCCTCAACCA

701 ACGTCCGCAGGATCTCCTCCGGTGTCCAGCGTTGCGTCTTGGCGACTTGC

751 AACACCTCGGCGGCGTTGCGGCGCACCGTGGCCAGCTTCAACCGCCGCAG

801 CGCCGCGTCAAGGTCAGCAGCCAGCGGTGCCGCCGAGGACGGTGCCACCG

851 GCTTGGCAGCGGTGGTCATGAGGCCGTCCCGTCGGTGGTGTTGATCTTGT

901 AGGCCTCCAACGAGCGGGTCTCGACGGTGGGCAGATCGAGCACGAGTGCG

951 TCGCCGGCGGGGCGGGGTTGTGGGGTGCCGGCGCCGGCGGCCAGGATCGA

1001 GCGCACGTCGGCAGCGCGGAACCGGCGAAACGCAACCGCCCGGCGCAGCG

1051 CGTCAATCAAAGCCTGTTCGCCGTGGGCGGCGCCAAGGCCGAGCAGAATG

1101 TCGAGTTCGGATTTCAGTCGGGTGTTGCCGATCGCAGCAGCACCGACGAG

1151 GAACTGCTGCGCTTCGGTTCCCAATGCGCAGAATCGTTTCTCTGCTTGGG

1201 TTTTCGGGCGAGGACCACGCGAGGGTGCGGGTCTGGGTCCGTCGTAGTGT

1251 TCATCGAGGATGGACACCTCACCTGGGCTGACGAGCTCGTGCTCGGCCAC

1301 GATCACACCGGTCGCAGGTTCCAACAGGATCAGGGCGCCATGATCGACCA

1351 CCACCGCCACGGTGGCACCGACGAGCCGCTGAGGCACCGAGTAACGAGCT

1401 GAGCCGTAACGGATGCACGAGAGGCCGTCGACCTTACGGCGCACCGACCC

1451 CGAGCCGATCGTCGGCCGCAGCGAGGGCAGCTCCCTCAAGACGGTGCGCT

1501 CGTCAACCAAGCGATCGTTGGGCACGGCGCAGATCTCCGAGTGGACCGTG

1551 GCATTGACCTCGGCGCACCATAGTTGCGCCTGGGCGTTGAGGGCACGTAG

1601 GTCGACCTGCTCACCGGCTAACGCAGCTTCGGTCAGCAGCGGCACCGCAA

1651 GGTCGTCCTGAGCGTAGCCACAGAGGTTCTCCACGATGCCCTTCGATTGC

1701 GGATCCGCACCGTGGCAGAAGTCCGGAACGAAGCCATAGTGGGACGCGAA

1751 TCGCACATAATCCGGTGTTGGAACAACAACATTGGCGACGACACCACCTT

1801 TGAGGCAGCCCATCCGGTCGGCCAGGATCTTGGCCGGAACCCCACCGATC

1851 GCCTCGAGGGCTTCGGCTATCATCGCCTGCGTGGTCGAGGCTTTCTCGTC

1901	GGCGGCGAACCGCTCAAACCGCCACCGCGAATAGGCCAGCTCCGCGCATA
1951	ACACCATCAGCCCCGGTGCCGCTTCGGCCCAATCCATCACCAGATAGTCA
2001	CCGGGTGACCAGACCGCCGGACGGCGTTGATGCCGGTTAGCGTTGCGCCA
2051	CCATACTTCCTGCTCGGCTACCAGGCGGCGGAAGTTACGGGCCGAGCCCT
2101	GATACCCGGCAGCTCGGGCGATCGGCAGCATCCGCTTCGCCGACATCTTG
2151	CCGTGTGATTTCTCGACTCGGGTGGCGACTAGATCGGTGAACGCGTCGAG
2201	GTTGCGTGGCCGTGGTTCCCGCGGGGGCGCGCCACCGGCCTCGGCCCGCT
2251	CGATGACCCGCTTGACCGTCTTGTGCGTACTACCGCACAGCTCGGCCGCG
2301	CCGCGATACGACCCGACCTGGTGATACGCCGAAATGATGTTCATACGCTC
2351	CCTTGCAGACTTCAATAGAGCTCCCTGGGCGGTGATCAAGTGACAGTTGG
2401	CGCTATCACCGTCACCGCCCAGGCCCTCAGCTCCCGGAAAAGACACGACG
2451	AGCCCGCTAAGGAGTGGGGACTTCTACCTGGCCACCAGTGGGGACTTCCT
2501	ACTGGCCACAGATGGGGACTTTCTCATGGCCATGGACATGCAC

(Total = 2543bp)

Sequence ID No.4 = IS*1612* negative strand to SEQ ID No.3.

1	GTGCATGTCCATGGCCATGAGAAAGTCCCCATCTGTGGCCAGTAGGAAGT
51	CCCCACTGGTGGCCAGGTAGAAGTCCCCACTCCTTAGCGGGCTCGTCGTG
101	TCTTTTCCGGGAGCTGAGGGCCTGGGCGGTGACGGTGATAGCGCCAACTG
151	TCACTTGATCACCGCCCAGGGAGCTCTATTGAAGTCTGCAAGGGAGCGTA
201	TGAACATCATTTCGGCGTATCACCAGGTCGGGTCGTATCGCGGCGCGGCC
251	GAGCTGTGCGGTAGTACGCACAAGACGGTCAAGCGGGTCATCGAGCGGGC
301	CGAGGCCGGTGGCGCGCCCCCGCGGGAACCACGGCCACGCAACCTCGACG
351	CGTTCACCGATCTAGTCGCCACCCGAGTCGAGAAATCACACGGCAAGATG
401	TCGGCGAAGCGGATGCTGCCGATCGCCCGAGCTGCCGGGTATCAGGGCTC
451	GGCCCGTAACTTCCGCCGCCTGGTAGCCGAGCAGGAAGTATGGTGGCGCA
501	ACGCTAACCGGCATCAACGCCGTCCGGCGGTCTGGTCACCCGGTGACTAT
551	CTGGTGATGGATTGGGCCGAAGCGGCACCGGGGCTGATGGTGTTATGCGC

601   GGAGCTGGCCTATTCGCGGTGGCGGTTTGAGCGGTTCGCCGCCGACGAGA

651   AAGCCTCGACCACGCAGGCGATGATAGCCGAAGCCCTCGAGGCGATCGGT

701   GGGGTTCCGGCCAAGATCCTGGCCGACCGGATGGGCTGCCTCAAAGGTGG

751   TGTCGTCGCCAATGTTGTTGTTCCAACACCGGATTATGTGCGATTCGCGT

801   CCCACTATGGCTTCGTTCCGGACTTCTGCCACGGTGCGGATCCGCAATCG

851   AAGGGCATCGTGGAGAACCTCTGTGGCTACGCTCAGGACGACCTTGCGGT

901   GCCGCTGCTGACCGAAGCTGCGTTAGCCGGTGAGCAGGTCGACCTACGTG

951   CCCTCAACGCCCAGGCGCAACTATGGTGCGCCGAGGTCAATGCCACGGTC

1001   CACTCGGAGATCTGCGCCGTGCCCAACGATCGCTTGGTTGACGAGCGCAC

1051   CGTCTTGAGGGAGCTGCCCTCGCTGCGGCCGACGATCGGCTCGGGGTCGG

1101   TGCGCCGTAAGGTCGACGGCCTCTCGTGCATCCGTTACGGCTCAGCTCGT

1151   TACTCGGTGCCTCAGCGGCTCGTCGGTGCCACCGTGGCGGTGGTGGTCGA

1201   TCATGGCGCCCTGATCCTGTTGGAACCTGCGACCGGTGTGATCGTGGCCG

1251   AGCACGAGCTCGTCAGCCCAGGTGAGGTGTCCATCCTCGATGAACACTAC

1301   GACGGACCCAGACCCGCACCCTCGCGTGGTCCTCGCCCGAAAACCCAAGC

1351   AGAGAAACGATTCTGCGCATTGGGAACCGAAGCGCAGCAGTTCCTCGTCG

1401   GTGCTGCTGCGATCGGCAACACCCGACTGAAATCCGAACTCGACATTCTG

1451   CTCGGCCTTGGCGCCGCCCACGGCGAACAGGCTTTGATTGACGCGCTGCG

1501   CCGGGCGGTTGCGTTTCGCCGGTTCCGCGCTGCCGACGTGCGCTCGATCC

1551   TGGCCGCCGGCGCCGGCACCCCACAACCCCGCCCCGCCGGCGACGCACTC

1601   GTGCTCGATCTGCCCACCGTCGAGACCCGCTCGTTGGAGGCCTACAAGAT

1651   CAACACCACCGACGGGACGGCCTCATGACCACCGCTGCCAAGCCGGTGGC

1701   ACCGTCCTCGGCGGCACCGCTGGCTGCTGACCTTGACGCGGCGCTGCGGC

1751   GGTTGAAGCTGGCCACGGTGCGCCGCAACGCCGCCGAGGTGTTGCAAGTC

1801   GCCAAGACGCAACGCTGGACACCGGAGGAGATCCTGCGGACGTTGGTTGA

1851   GGCCGAGATCGCTGCCCGCGATGCCTCCAACACCGCCAACCGTCTCAAGG

1901   CCGCAGCCTTCCCGGTCACCAAGACCCTCGACGGGTTCGACGTCACCGGA

1951   TCGTCGATCACCGCAGCCACGTTCGACTACCTGTCGAGCCTGGAATGGAT

2001   TCGGGCACAACAGAACCTGGCGGTCATTGGCCCACCTGGTACGGGCAAAA

2051   GTCACCTGCTCATCGGCTGCGGGCACGCTGCCGTCCACGCCGGATTCAAA

2101   GTCCGCTACTTCACCGCCGCCGACCTGATCGAGGTCCTCTACCGCGGCCT

2151   GGCCGACAACACCGTCGGCAAGATCATCGACACCCTGCTCCGCGCGGATC

2201   TGGTCATCTTGGACGAGATCGGCTTCGCCCCGCTCGACGACACCGGGACT

2251   CAACTGTTGTTCCGGCTCGTGGCTGCCGGCTACGAGCGCCGCTCCCTGGC

2301   CATCGCCTCGCATTGGCCCTTCGAACAATGGGGGCGATTCCTGCCCGAGC

2351   ACACCACCGCCGCCAGCATCCTCGATCGGCTGCTGCACCACGCCAGCATC

2401   GTCGTCACCTCCGGCGAGTCCTACCGGATGCGCCACGCCGACCACAAGAA

2451   GGGAGCCGCCAAGAATTAGCCAACCACCCGCAGCGGAGTGGGGACTTCTG

2501   CTGGCCACCAGCGGGGACTTCTACTTGGCCATTGACAGTGCAT

(Total = 2543bp)

Sequence ID No.5 = Amino acid sequence of polypeptide designated istA
              encoded by Seq ID No.4.

1   VSFPGAEGLGGDGDSANCHLITAQGALLKSARERMNIISAYHQVGSYRGA

51   AELCGSTHKTVKRVIERAEAGGAPPREPRPRNLDAFTDLVATRVEKSHGK

101   MSAKRMLPIARAAGYQGSARNFRRLVAEQEVWWRNANRHQRRPAVWSPGD

151   YLVMDWAEAAPGLMVLCAELAYSRWRFERFAADEKASTTQAMIAEALEAI

201   GGVPAKILADRMGCLKGGVVANVVVPTPDYVRFASHYGFVPDFCHGADPQ

251   SKGIVENLCGYAQDDLAVPLLTEAALAGEQVDLRALNAQAQLWCAEVNAT

301   VHSEICAVPNDRLVDERTVLRELPSLRPTIGSGSVRRKVDGLSCIRYGSA

351   RYSVPQRLVGATVAVVVDHGALILLEPATGVIVAEHELVSPGEVSILDEH

401   YDGPRPAPSRGPRPKTQAEKRFCALGTEAQQFLVGAAAIGNTRLKSELDI

451   LLGLGAAHGEQALIDALRRAVAFRRFRAADVRSILAAGAGTPQPRPAGDA

501   LVLDLPTVETRSLEAYKINTTDGTAS

(Total = 526 aa)

Coded by nucleotides 98 - 1678 of seq ID No 4.